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913 + 1.092824 homo sapiens (human)
27 | 1.15725 rattus norvegicus (rat)
595 | 128408 homo sapiens (human)
335 | 125444 homo sapiens (human)
3672 | 1.01113 caencrhabdi'is elega
277 | 1.4189 homo sapiens (Euman)
274 | 1.4189 homo sapiens (Euman)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ' Qa4628 plasmodium berghei (s
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                                                                                                                                  -MODEL-trames_nipodel -DEV-xlp
-Q-ZGqnillYSPTO spool/MSDOCEFONE (Final_Lin4) KDV.] KDX GLIDPAGAPP_query fastill 2017
-DE-SWissProt. 39 -GPMT (astan -SMPPIX.ersp -GAPOP-12 000
-QAPEXT-4,000 -MINMATCH-0, 100 -LOMBOT-0 000 -LOMBOT-0,000
-QAPOP-4 SQU -QAPEXI-0 050 -VARDOU-10 000 -VQAPEXT-0,500
-FGAPOP-5,000 -FGAPEXI-7 000 -VARDOU-10,000 -VGAPEXT-0,500
                                                                    About: Results were produced by the GenGore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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out_format : pfs
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-TRANS-bumman40.edi -LIST-45 -DOYALIGN 200 THE_SCOPE pet
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -Mucbe-LOCAL -OUTFMI-pfs
OM of: US-09-525-998A-11 to: SwissProt_39:*
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Database length: 36664827
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Query length: 600
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                                                                                                                     Command line parameters:
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733 : P21849 giardia lamblia (g. 555 : P25122 homo sapiens (huma 1712 : "Offolfs Lattus notreations (g. 575 : 1956/88 Artugus lattus norvegicus (r. 779 : 19712) rattus norvegicus (r.
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Getanaya T., Granger G.A., Lentz R., Erab H., Kohr W.J., Goeddel D.V.,
"Molecular cloning and expression of a receptor for human tumor
mecrosis factor."
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MEDITHE SIGNATOR SECTION PROMISES AND SECTION SIGNATURE. FOR SECTION SIGNATOR SECTION 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Ref. 17, freated)
01-FEB-1991 (Ref. 17, fast segmence apdate)
20-AUG-2001 (Ref. 146, fast annotation update)
EMPOR MEDICAL RECEPTOR FECULATION FACTOR NECES FACTOR
BINDING FR.TEIR 1) (IMP. (16.0) (IMP.KL) (IMP. EL) (15.0) (CLLOA).
INFRREIA OR INFRI OR INFAR.
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Mammalias Eutherias Primatess Cafarrhinis Huminidaes Homos
NCBL_TaxID-9606;
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Forth F., Siroli S., Danish M., Hingler A., Ambros P.F.,
"Strandar of the London TME recept in (pG) wene (TMFR) and
Localization of the Mondar Lipids.";
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MITCHE (1375 ) LLAMBELLY (74)
CLAY PLWE, Rainett E., Chants; Le lutter M., Eudmen M.;
CLAY PLWE, Bainett E., Chants; Lector (INI) receptor cONA-expression of recombinatisolute INF-16dict Frotelia";
Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
SwissProt_39:1584_C181A - 117.50 172.95 0:0092
SwissProt_39:1784_HUMAH - 117.50 164.49 0:0095
SwissProt_39:170Fa - 117.00 164.65 0:0111
SwissProt_39:DLD.Z.XBAA - 116.00 177.77 0:0115
swissFrot_39:DLIs_KAI - 116.00 177.77 0:0112
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P19438;
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This SWISS-PROT entry is copyright. It is produced through a collaboration the swiss Institute of Bioinformatics and the BMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cuttics requires a license afterment (See http://www.isb-sib.ch/anneanneg/or send an email to license*isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR THE ALPHA. THE ADAPTOR MOLECULE FADD RECEPTOR. THE RESULTING RECRUITS CASPAGE. BT OF THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTECLYTIC ACTIVATION WHICH INTITATES THE SUBSEQUENT CASCARSE (ASTARTARE SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPPOSIS. CONTRIBUTES TO THE INDUCTION OF NOWEYTOCIDAL THE FFECTS INCLUDING ANII-VIRAL STATE AND ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBGUIT: THE BINDING TO THE EXTRACELLULAR DOMAIN OF THERI LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERPRETS SPECTFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD. INTERACTING PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD. ARE RECRUITED TO THERE COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF KAPPA B SIGNALING
                                                                                                                                                          X-RAY CHYSTALLOCRAPHY (2.95 ANCSTROMS) OF 30-211 IN COMPLEX WITH THPB. MEDINE HEADON DIMENSPRAY;
BEOGER C., LOELSCHEI, LESSLAUER W.;
Crystal structure of the soluble human 55 kd TNF receptor human TNF beta complex: implications for TNF receptor activation.";
CC1 73:431-445(1931).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCRIBULAR INCATION: TYPE I MEMBRANE PROTEIN.

DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROPABLY IDENTICAL TO
THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
                                    Engelmann H., Novick D., Wailach D.; Warwe tunner necrosis factor binding proteins purified from human urine. Evidence for immunological cross reactivity with ceil surface tunner necrosis factor resceptors.";
                                                                                                                                                                                                                                                                                                                                                               Naismith J.H., Devine T.Q., Khono H , Sprang S P . "Structures of the extracellular domain of the type I tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
SIMILARITY: CONTAINS A LA-NGFR/TNFF-TYPE CYSTEINE-KICH REGION.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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WWW-"bttp://www nebi.nim nih.gov/prow/ed/ed120a.html.
                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1 R5 ANGSTROMS) OF 41-202
                                                                                                                    Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                            MEDLINE-97094982; PubMed-8939750;
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M75864; AAA61201.1; JOINED.
M75865; AAA61201.1; JOINED.
M60275; AAA36756.1; ...
A21522; CAA01558.1; ...
                     MEDIINE-90110215; PubMed-2153136;
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1 NCF; 07-DEC-95,
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S12057; S12057.
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SEQUENCE OF 41-45.
                                                                                                                                                                                                                                                                                                                                                                                                          factor receptor."
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TUMOR NECROSIS FACTOR RECEPTOR 1.
TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
                                                                           PROSITE, PS50017, DEATH_DOMAIN; 1.
Receptor, Iransmembrane, Glycoprotein, Repeat) Signal, Apoptosis;
3D-structure.
                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MISSING (IN REF. 4).
                                                                                                                                                                                                   TNER-CYS 4.
N-SMASE ACTIVATION DOMAIN (NSD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 euGlyAspargGlutysArgAspScrValCysDioGluGlyLstyrHe 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AIGGGTTTTTCATTGTTTTATTGTTGTTGTTGGTGGTGTTTGGA 50
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4CEFBA96D03B8225 CRC64;
                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 94.787
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TNFR-CYS 2.
TNFR-CYS 3.
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                                                        PROSITE; PSDOK52; TNFP_NGFR_1; 3. PROSITE; PS50050; TNFP_NGFR_2; 3.
InterPro: IPRO01368; TNFR_c6
Piam; PF00531; death; 1.
Pfam; PF00020; TNFK_c6; 4.
ProDom; PD000771; TNFR_c6; 1.
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SMARL; SMUUOOS; INFR; 4.
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Ratio: 5.588
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DISULPID
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REPEAT
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PECPETITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING RECEPTOR CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-TODICING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 POTTOTING TOTAL WHICH INTITATES THE SUBSEQUENT CASCADE OF CASPASES (ASTARIATE-SPECIFIC CYSTEINE PROTECTIVE ACTIVATION WHICH INTITATES THE PROTECTIVE CASPASES) MEDIALING APOPTOSIS (HY SIMILARITY) OF THERE INDIVING TO THE EXTRACELLULAR DOMAIN OF THE EXCEPTORS EAST. LOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THE FELSEFORS EAST. LOMAINS PROTEINS SUCH AS TRAPS, RIP AND POSSIBLY FADD, ARE RECRUITED TO THEF IN COMPLEX ACTIVATES AT TWO DISCINIC SIGNALING CASCADES. APOPTOSIS AND NF-KAPPA B STORMLING (PY SIGNALING CASCADES. APOPTOSIS AND SUCH AS TRAPS, TWO DISCINIC SIGNALING CASCADES. APOPTOSIS AND STRAPS A STORMLING SOUTH AND METRAPPARE SOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AND METRAPPARE SOCIATION AND METRAPPARE SOCIATION AND METRAPPARE SOCIATION. TYPE I MEMBRANE PROTEIN.
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10-OrT-1996 (Pel 34, Last ancetation update)
20-AUG 2091 (Pel 40, Last ancetation update)
TUMOR NECEOSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrola (Pig).
Bukaryola, Meladda, Chariata, Verlebrata, Enteleostomi,
Mammalia, Eutheria, Cetartiedactyla: Stina; Suidae, Sus
218 GIBAGAGGGGIGCTICACGGTTCASAAAACCACCICAGACACTGCCTC 267
                      268 AGTIGCTCCAAATGCCGAAAGGAAAIGCGICAGGTGGAGATGTTCTTG 317
                                                                                                          101 SerCysSerLysCysArgLysCluMetClyClnValClu1:eSerSerCy 117
                                                                                                                                                                    318 CACAGIGGACGGGGACACGIGTGIGGCIGCAGGAGAACAGACGGG 367
                                                                                                                                                                                                                                                         ATTALLIGGAGTGAAAAGCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 417
                                                                                                                                                                                                                                                                             468 CTGCCATGCCAGGTTTCTTTCTAAGAGAAAAAGGGTGTGTCTGTAGTA 517
                                                                                                                                                                                                                                                                                                                                                                                                                                             518 ACIGTAAGAAAAGCCTGGAGTGCACGAAGTTGTGCTTACCCCAGATTGAG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 sthrValAspArgAspthrValCysGlyCysArglysAsnGlnlyrArgH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 AATGTTAAGGGCACTGAGGAGTCAGGCACCACA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AshVallysGlyftrGluAspSerClyfthr 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96011645; PubMed-7590278;
Suter B., Pauli U.H.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: SwissProt_39:INR1_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID TNRI_PIG SIANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163:263-266(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor."
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P50555;
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This SWISS PROFERRING IS COPYTIGHT, IT is produced "Lond a collaboration between the SWISS Institute of Bioinformatics and "Le EMBL outstation—the European Busintormatics Institutions is Institutional to the as is content is in no way modified and this statement is not removed. Usage by and for commercial collaboration is the removed. Usage by and for commercial collaboration and an email to inchaefish subject.
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HY SIM
                                                                                                                                                                                                                                                                                                                                                                       CD72361ECFOCOD4 (CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFR-CYS 4.
INFR-CYS 4.
N-SMASE ATTIVATION DOMAIN (NSD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYTOPLASMIC (F-TENTIAL)
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Percent identity: 69,658
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                                                                                                                                                                                                    HSSP: P19438; IINR.
InterPro: IPEGGG188; Death.
InterPro: IPEGG198; INFR_66.
                                                                                                                                                                                                                                                                 Pfam: PFOC5.1: death. 1.
Plam: PFOC6.2: INFR ccf. 3.
Proton: FLOGUOZZI. INFR-ccf. 1.
SMART: SMO0005: DEATH. 1.
SMART: SMO0005: INFR. 3.
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01-MAY-1992 (Rel. 22, Greated)
01-MAY-1992 (Rel. 22, Last scription, plate)
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IUMOR NETROSIS FACTOR PEREPTOR 1 PRECURSOR (PAG) (TNF-P1) (TNF-R1)
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Bukaryota, Metamoa, Chordata, Cramiata, Vertebiata, Esteleostomi,
Mammalla: Butheria: Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodwin R G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
"Molecular gloning and expression of the type 1 and type 2 marine
receptors for tumor necrosis factor."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor receptors demonstrate one receptor is species specific.";
                                                           118 CACCCTCAAAATAATTCGATLIGGGGAGAAGGAAGGAACTA 167
                                                                                                                                                                                 168 CITICIACAATGACTGT777AGG7777G777AGGATTAGGGACTT27AGGGACT 217
                                                                                                                                                                                                                                                                                                                                268 AGCIGCICCAAAIGCCGAAAGGAAAIGGGICAGGIGGAGAICICIICIIG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 ATTATIGGAGIGAAAACTITICCAGIGGIICAALIGCAGCCICIGCCIC 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    468 CTGCCATGCAGGTTTTTTTTTAAGAAAAGGAGTGTGTGTCCTGTAGTA 517
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                                                                                                                                                                                                                                                                                              218 GIGAGAGOGGCICCTICACCGCTICAGAAAACCACGICAGACACIGCCIC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 nCysHisSerGlyPhePheLeuArqAspL,sGluC,sValSerC,sValA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 ACTGTAAGAAAAGCCTGGAGTGAAAAHHGTGTGACTAGCCCCAGATTGAG 567
                                                                                                                                                                                                          34 roclyAspangolulpsAngOluScrittLCysPtuGlnGlyDysTynScr 50
                                                                                                                      51 HisProGlaAsnArqSerIleCysCysThrLysCysHisLysClyThrTy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 AAIGTTAAGGGCACTGAGGACTCAGGCACCACA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 ThrArgAsnAspPheGlnAspThrGlyThrThr 210
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ID TNRL_MOUSE STANDARD;
AC P25118;
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                                                                                                                                                   Mothe J.G., Brockhaus M., Gentz.R., Losslauer W.;
"Molecular cloning and expression of the mouse Infraeeptor type b.";
Immunogenetics 34:338-340(1991).
                                                                     'Cloning, expression and cross-linking analysis of the murine p55
                               MEDLINE-91285014; PubMed=1647956;
Batrett, K., Taylor Fishwick D.A., Cope A.P., Kissonerqhis A.M.,
Gray P.W., Peldmann M., Foxwell B.M.J.;
                                                                                                                                                                                                                                        "Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.", \  \  \,
                                                                                 tumor necrosis factor receptor.";
Eur. J. Immunol. 21.1649-1656(1991).
. Seli, Biol, 11.3020-3026(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, M59377; AAA40464.1,
EMBL, X59288; CAA441922.1,
EMBL, 126349; AAA5936.1;
EMBL, 126349; AAA5936.1;
EMBL, M70656; AAA40465.1;
EMBL, M70657; AAA40465.1; JOINED.
                                                                                                                                        MEDLINE-92039815; PubMed-1657766;
                                                                                                                                                                                                                                                                                                   MEDLINE-93156721; PubMed-8381516;
                                                                                                                                                                                                                 MEDLINE 94245292, PubMcd-8188324;
Bebo B.F., Linthicum D.S.;
                                                                                                                                                                                                                                                                Immunogenet.cs 39:450-451(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1314884; Tnirsfla.
InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
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Pfam; PF00020; TNPR_c6; 4.
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PIR, S16677, S16677.
PIP, S19021, S19021.
                     SEQUENCE FROM N.A.
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                                                                                                                   SEQUENCE FROM N.A.
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N. LINKED (GLUNAC. ..) (POIENTIAL).
                                                                                                                                           Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis. SiGNAL, 1 21 POTENTIAL.
                                                                                                                                                                                            IUMOR NECESSIS FACTOR RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                               N-SMASE ACTIVATION DOMAIN (NSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 CITGIACAAIGACIGIOCANNOCONGGAGAAIACNAACIGGAGGAAGI 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 GTGAGAGGGGCTCCTCACCGCTTCAGAAAACCACCTCAGAGACTGCCTC 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 167
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                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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07190286302869 CR064;
                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
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82.464 Percent Identity: 66.351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GCIGITGGGGGGGAAIAIACCCTICAGGGGTIAITATIGGA
                                                                                                                                                                                                                                                                                                                                        TNFR-CYS 2.
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                                                                                                                     PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                    PROSITE; PS0052; TNFR_NGFR_1; 3. PROSITE; PS50050; TNFR_NGFR_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50129 MW:
ProDom; PD000771; TNFR_c6; 1.
SMART; SM00005; DFATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-525-998A-11 x TNR1_MOTISE
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                                                                                                                                                                                                                                                                                                                                     454 AA;
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MEDITAR 91970841. Fifthed 1701091.

A Himmler A., Maurer Fooy I., Kroenke M., Scheurich P., Filtermaier K., Almmler A., Maurer Fooy I., Kroenke M., Scheurich P., Filtermaier K., Almmler A., Maurer Fooy I., Broenke M., Scheurich P., Filtermaier K., Lantz M., Olsson I., Hauptmann R., Stratowa I., Adolf 918.

I molecular closuig and expression of human and rat tumor necrosis factor-binding protein. ", DNA Call Biol, 91705-715(1997).

IL DNA Call Biol, 91705-715(1997).

IL DNA Call Biol, 91705-715(1997).

PERFECTE CALLED THE DRAIN HIDDING MEDETTR THE RESULING SCHOOLSK (DISC) PERFORMS CASTASE-8 PROTEOTING OFFICE THE RESULING AGGREGATE CALLED THE DRAIN HIDDING NEIGHT STREET THE PROTEOTING CASTABLE SCHOOLSK (DISC) PREFORMS CASTASE-8 PROTEOTING CASTABLE SHOW SHOW TRIED THE EXTRACLIDAR FURALLY PRACTICE THE FRONTES THE EXTRACLIDAR FURALLY DRAINS TO THE EXTRACLIDAR FURALLY DRAINS THE PLAIN DOMAIN OF TRAINS THE PROTEOTING AND THE PRACTICE THE DRAINS THE PROTEOTING AND THE PRACTICE THE DRAINS THE PROTEOTING AND THE PRACTICE THE DRAINS THE PROTEOTING AND THE PRACTICE THE PROTEOTING AND THE 
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-1. SUBCRITIONAL CONTROL TYPE I MEMPHRANE PROTEIN.

SIMILARITY, SANIANS A DA MORENINE PROTEIN.

SIMILARITY: CANTAINS A DA MORENINE.
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Mammalla: Estheria: Rodentia: Scharoquathi, Muridae, Muridae; Rattus.
NGRI,19v1D-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Re). 19, Created)
02-AMR 2792 (Pc) 22, Last sequence update)
20-AUG-2001 (Rei, 40, Last amiotation update)
1985E HESPOST FACTOR EFFERTOR (Pco) (INF RI) (INF-RI)
                                                                                                    318 CACASTGGACCOGGACACGISTGGCIGCAGAAAGAACLAGIACGGC 367
                                                                                                                                                                                                                                                                              518 ACTOTAAGAAAQPCTGGAGTACAAGTTGTGPPTA...PPPCAGATT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 is Cystystys AradiadlacysMettystoucystou ProProProLeu 200
                                                                                                                                                                     117 schrataAsptysAspthrValCysGlyCystysGluAshJinPheGluA 134
                                                                                                                                                                                                                                      368 ATTATTGGAGTGTTTTGCAGTGGTTGAATLGGAGGCTCTGGGTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 CIGGLAIGDAGGLIIGHIGIAAGAAAAACGAGIGIGILIGGLAGIA 517
565 GAGAATGITAAGGGGACTGAGGACTGAGGCAA7
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ID TNR1_kAT SIANDARD;
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non-profit institutions as long as its content

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modified and this statement is not removed. Usage by and for commercial
                entities requires a license agreement (See http://www.isb sib.ch/announce;
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                PROSTTE; PS00662; TNFR NGFR_1; 3.
PROSTTE; PS50050; TNFR_NGFR_2; 3.
PROSTTE; PS50017; DEATH_DOMAIN: 1.
Receptor, Transmembranc, Glycoprotein, Kepraf, Signal, Apoptosis.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                  IUMOR NECROSIS FACTOR RECEPTOR 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 CACCCHCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 ......GATAGTGTGTGTGCCCAAGGAAAATATATC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGGGCCTCTCCACCCTGCTGACCTGCTGCTGCTGCTGCTCCTGGA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGlyLeuProIleValFroGlyLeuLeuLeuSerLeuValLeuLeuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 cuGlyAspArgClutysArgAspAsnLcuCysProClnClytySlyrAla 50
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                                                                                                                                                                                                                                                                                                                               POTENTIAL,
CYTOPLASMIC (POTENTIAL).
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FNFR-CYS 3.
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                                                                                                                           InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                      Profom; PD000771; TNFR_c6; 1.
                                                             EMBL: M63122; AAA42256.1; -.
                                                                                                          InterPro; IPRO00488; Death
                                                                                                                                         Pfam: PF00531; death; 1. Pfam: PF00020; INFR_c6; 4.
                                                                                                                                                                                      SMART; SM00005; DEATH; 1
SMART; SM00208; INFR; 3.
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                                                                            PIR; B36555; B36555.
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SUBMITTED (FEB-1997) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: KECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPARSE B TO THE ACTIVATED RECEPTOR. THE RESULTING ACCRECATE CALLED THE DEATH INDUCING SIGNALING COMPLIX (DISC) PERFORMS CASPASE-8 PROPEDLYTIC ACTIVATION WHICH INTITIATES THE SUBSCIOUNE CASCAGE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPIOSIS (BY SIMILARITY).

1- SUBGNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFRI LEADS TO HOMOTE MAGNICAL THE RECEPTORS DEATH DOMAINS PROFIT THE RECEPTORS DEATH DOMAINS WITH THE DEATH DOMAIN OF TRAND. VARIOUS TRAND-INTERACINED DOMAIN OF TRAND. VARIOUS TRAND-INTERACINED TO PROFIT SOURCE AS TRANS. RIP AND POSSIBLY FAID). ARE REFRUITED TOWNERS THERE COMPLEX
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TOWDE NECHOESTS FACTOR RECENTOR 1 PRECISES (FGO) (TRE R1) (INF R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodaetyla, Ruminantia, Pecera, Hovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee E.-K., Talyor M.J., Kehrli M.E.;
"Cloning of cDNA encoding bovine tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                     467
                                                                                                                                   84 ysAspLysGlyThrPheThrAlaSerGlnAsnHisValArqGlnCysLeu 100
                                                                                                                                                                                268 AGCTGCTCCAAATGCCGAAAGGAAATGGGTGAGGTGGAGATCTCTTGTTG 317
                                                                                                                                                                                                          SerCysLysThrCysArgLysGluMetPheGlnValGluIleSerProCy 117
                                                                                                                                                                                                                                                                       318 CACAGIGGACCGGGACACTGTGTGTGTGCAGGAAGAACCAGIACCGGC 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEM C'ELGIACAMIGACTGTC'ANGROCCEGGGCAGGAIACGGACGGGAGT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 nCysHisAlaGlyPhePheLeuSerGlyAsnGluCysThrProCysSerH 184
                       218 GTGAGAGGGGTCC1 FCACGGCTTCAGAAAACCACCICAGACACIGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 AsnValThrAsnProGlnAspSerGlyThr 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-A05-2001 (Rel. 40, Created)
20-A0G-2001 (Rel. 40, Last sequ
20-A0G-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: SwissProt_39:TNR1_BOVIN
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019131;
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BY SIM
                                 -t- SIMITARITY; CONTAINS A LA-NGER/TNER-TYPE CYSTEINE-RICH REGION.
-t- SIMILARITY; CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane, Glycoprotein, Repeat, Signal, Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NETROSIS FACTOR PETERIOR 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
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                    SUBCELLULAR LOCATION TYPE I MEMBRANE PROFEIN.
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NP-KAPPA B SIGNALING (BY SIMILARITY).
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PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                            Pfam: PF00531; death; 1.
Pfam: PF00020; TNFR c6; 3.
Probom: P10000771; TNFR_c6; 1.
SMART: SM00005; DEATH; 1.
SMART: SM00208; TNFR; 3.
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                                                                                                                                                                                                                                                                                                                    InterPro; IPR000488; Death.
InterPro; IPR001368; INFR_c6.
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SIGNAL
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Percent Identity: 64.455
  Length:
                                                                   US-09-525-998A-11 x INRI_BOVIN
4.568
                           80.045
 Chality
                         Percent Similarity:
               Rat.io:
                                                      alignment_block:
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Align seq 1/1 to: INRL_BoVIN from: 1 to: 471

51 GCTGTTGGTGGGAATATATACCCTCAGGGGTTATTGGA

Crowe P.B., van Arsdale J.L., Walter B.N., Water C.F., Hession C., Ehrenfels B., Frowning J.L., Din W.S., Goodwan R.G., Seith C.A.,

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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
1.VARC-20A1 (Bel. 44, Last annotation update)
1.VARRHOTOXIN-BETA RECEPTOR PRECURSING (TUMOR NICROSIS FACTOR PROCEPTOR
2. MELATED PROTEIN) (TUMOR NECKOSIS FACTOR C RECEPTOR).
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Mammalia: Eutheria: Primates: Qatarihini: Hominidue: Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 ATTATTGGAGTGAAAAGGTTTGGAGTGGAATTGGAGGTGGGG 417
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                                                                                                                                                                                                    168 CHGIACAATGA TGLCCAGGCCGGGGCAGGAIACGAA LGCAGGAGT 217
34 rodlyAspLeadluLysArqGluSerProCysFroGluditislyiAsu 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 GIGAGAGGGGGIFGIICACCGGGTTCAGAAAACCACCIFABAAAAGGGGTC
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MEDLINE-93252381; Pubmed-8486360;
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This SWISS-PROT entry is orgyright It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BRH, outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afreement (See http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch)
                            -! - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA, POSSIBLE FUNCTION IN
                                                                           SIMILARITY: CONTAINS A LA-NGFP/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 ...GATAGIGIGI.....CCCCAAGGAAAAIAIACCACCCICAAAA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 GCCACTGGTGGTGGTGTGTTGGTGGGAAIAIACCCGGGGGTTA 82
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                                                                                                                                                                                                                                                                                                                                                                                                        LYMPHOTOXIN-BETA RECEPTOR. EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                              Receptor: Transmembrane: Glycoprotein: Repeat: Signal.
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                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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"A lymphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
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TNFR-CYS 4.
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Ptam; PF00020; TNFR_c6; 4.
ProDom; PD000771; PNFR_c6; 1.
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                                              IMMUNE DEVELOPMENT.
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Ratio:
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Kitson J., Raven T., Jianq Y.-P., Goeddel D.V., Giles K.M., Pun K. T., Griham C.J., Brown R., Faltow S.N.,
A death domain-containing receptor that mediates apoptosis.";
Nature 384:372-375(1996).
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PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Verfebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=97081063; PubMed-8875942;
Chinnaiyan A M . O'Rourke K , Yn G -L , Tynns R H , Garg M.,
Duan D.K., Xing i... Gentz R., Ni J., Dixit V.M.,
"Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WSLI_HUMAN STANDARD; PRT; 417 AA.
Q99830; Q94846, Q94044, Q950483, P78515; Q940831, Q99722, F78507;
Q99830;
                                                                                                                                                                                                                                229 TOCTTCACOCCITCAGAAAACACACICAGACACIGGGGGGGGGCCCAA 278
                                                                                                                                                                                                                                                                                                                                                                             229 ATGCCGAAAGAAATGGGTCAGGTGGAATGTGTTCTTGGAGAGTGGAGG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 rqLysThrGlnCysArqCysGlnProGlyMetPheCysAlaAlaTrpAla 136
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                                                                        179 ACTGTCCAGGCCCGGGGCAGGATACGGACTGCAGGGGGGTGTGAGAGCGGC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 ysValProCysLysAlaGlyHisPhe.....GlnAsnThrSerSerPro 181
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55 sArg...IleCysCysSerArgCysProProGlyThrTyrValSerAlaL 71
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                                                                                                                                                71 yscys...SerArglleArgAspThrValCysAlaThrCysAlaGluAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 TGTAGTAATTGTAAGAAAAGOTTGGAGTGGAGGAAGTTGTGGOTTAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       561 GATTGAGAATGTTAAGGGGAGAGAGAGTGAGGCACCACA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 .ValGluAlaAlaProGlyThrAlaGlnSerAspThrThr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR OF DEATH) (LARD).
THERSF12 OF WELL OF WSL OR APO3 OR DR3 OR DDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lymphoid;
MEDLINE=9708861/; PubMed 8934525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: SwissProt_39:wSL1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-LUÖL (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 GCACC
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EMBL: 075381; AAF51193.1; EMBL: 083597; AAB41432.1;

HSSP; P19438; LINK.

MIM: 603366;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NF-KAPPAB). DIRECTLY INTERACTS WITH TRADD ADAPTATOR MOLECULE, MAY PLAY A POLE IN PEGULATION LYMPHOCYTE HOMEOSTASIS SUBUNIT: HOMODIMER, INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE INFR1-ASSOCIATED MOGLECULE, TRADD AND THE TWREI RECEPTOR TO ACTIVATE ALLEAST HWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaudhary P.M., Hood L.E.;
Submitted (JAN-1997) to the EMBL/ScarRank/STRL databases
-!- FUNCTION: INDUCES APOPROSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Frain, and Petal lung;
MHDLINE-2026333; Pubmed-20293;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
Browning J.L., Macdonald H.R., Tschopp J.,
French L.E.,
French L., Macdonald H.R., Tschopp J.,
French L.E.,
HEAMP, a novel apoptosis-mediating receptor with sequence homology
to tumor necrosis farter receptor 1 and Pas(Apo-1/CD95).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NETAPPA B SIGNALING.

STREELLULAR LOCATION TYPE I MEMBRANE PROTEIN (POTENTIAL).

ALTERNATIVE PRODUCTS: 4 ISOFORMS, WST-1/LARD-1A (SHOWN HERE),
WSL-SI/LARD-3 AND WSL-S2. ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECTFOTIVE AMINDARILY EXPRESSED IN THYMCYTYPE AND
LYMPHCKYTES, DETECTED IN LYMPHCKYTES AND
LYMPHCKYTES, DETECTED IN LYMPHCKYTES BOOTON, INTESTINE, AND SPLEEN, ALSO FOUND IN THE PROSIATE.

PTM: GLYCOSYLAND C PROBABLED.

SIMILARITY: CONTAINS A LA NEFE/LINE-TYPE CYSTEINE-FICH RESION.
                                                                              SEQUENCE FROM N.A. Lin W.S., Cosman D., Smith C.A., Goodwin R.G.; Submitted (JAN-1997) to the FMR Georgank/ThPRT databases
                                                                                                                                                                                                                                                                                                                                                        MEDELINE-G7148200. PubMed-R444812.
Marshers S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Ashkorazi A.;
Goddard A.D., Bauer K.D., Ashkorazi A.;
Apo S. a new month of the tumor necrosis factor receptor family, contains a death domain and activates apoptusis and NF-kappa-B.;
Curr. Biol. 6:1669-1676(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screaton G.R., Xu X.-N., olsen A.L., Cowper A.E., Tan R., McMichael A.J., Bell J.L.; fill all and lympheid for the fill domain containing receptor requiated by alternative pre-mENA splicing."; Proc. Natl. Acad. Sci. H. S. A. 94.4615-4619(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2273, Purmed 9114239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 4-417 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 7-417 FROM N.A.
Science 274:990-992(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunity 6:79-88(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain·
                                                                                                                                                                                                                                                                                                                                     IISSUE-Hoart
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STLUSSTPEPPÄAAVTIWP, WPWW, VLLASLAVPELLUS ...
VLGFGARGWEGSEREAWHELLHIEFLLASYARGYGR (IN
                                                                                                                                                                                                                                                                                                                                                                        MEWVOVILLAGLIVYSTU LGA ITTYYPHOWPHYPLY LALAFAG
MEALLPPPATHLS + SPWMAGNAPSFLOMORGEAGERGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D AN SCREENING DAMERIZATION, AND INRI INFRACTION.

P PF > AG (IN REF. 6).

P > L (IN REF. 7).

P > L (IN REF. 1).

A > E (IN REF. 1).

A > E (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                  1-5A: SUPPRISSES H-MOLIMERIZATION, THERI
HATHRACITON, AM AN HETGOLY BROSCHON.
1-5A: SUPPRISSES H-MOLIMERIZATION, AND
THERI INTERACITON.
                                                                                        TRESTER ESCOCTO, THERESTER T. 2.
PROSTER ESSOCTO, THERETO, 1.
PROSTER ESSOCTO, DEATH DOWAIN, 1.
RECEPTOR: Apoptosis, Alternative splicing, Dansmombrancy Signal.
                                                                                                                                                                                                                                                                                              N LINKED (GLENAR, . .) (PETENTIAL). N-LINKED (GLENAR, . .) (PETENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               NIPTPTSCEQCESSECSWLALWSPSCLUPP (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 TGTGTGTCCCCCAAGGAAATATATCCACCCTCAAAATAATFCAATTTGCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 GTACCAAGIGCCACAAAAGAAACTAQIIGIACAAIGACDGIC AGGCCG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 ysArdGlyCysProAladlyHisTyrLeuLysAlaProCys111 31.Pro 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CICCIGGACCIGILISGIOSGAAIAIACCCCICAGOGGILALL DAGALAG 92
                                                                                                                                                                                                                                                                                                                                                             MISSING (IN ISCHORM WSI-SI).
                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM WELS.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 OArgCysAspCysAlaGlyAspPheBisLysLysTleGlyLenFheCysC
                                                                                                                                                                      WSL I PROTEIN.
EXTRACELLULAR (P. 1ENLIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5226319DFDB46706 CRC64;
                                                                                                                                                                                               FIENTIAL.
OYESPLASMIC (PRENITAL).
                                                                                                                                                                                                                                                                                                                                                                                                            ISOFORM WSL S2)
                                                                                                                                                                                                                                                                                                                                               ISOFORM WSL-SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.839 Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aliqueseq 1/1 to. WSL1_HUMAN Irom: 1 to: 417
                                                                                                                                                                                                                      4 X INFR-CYS.
                                                                                                                                                                                                                                   INFR CTS 1.
                                                                                                                                                                                                                                                                     INFR-CYS 4.
                                                                                                                                                                                                                                                           TNFR-CYS 3.
                                                                                                                                                                                                                                                                                     DEATH.
                                            InterPro, IPRO00488; Death.
InterPro, IPRU01358; INFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15385 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-525 998A 11 x WSLL_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouality: 209,50
Ratio. 2.054
Percent Similarity: 54,839
                                                                                    INFR (16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
312
570
381
                                                                                                                                                                                                                                                                                                                                                                                                                                                           356
                                                                      Pfam: PF00531; death:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4381
381
4381
AA:
                                                                                 PF00020:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aliqnment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                         VARSPILIS
VARSPILIS
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
MUTAGEN
                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                        VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFILICT
                                                                                                                                                                                                        DOMA IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGER
                                                                                                                                                Repeat.
SIGNAL
                                                                                                                                                                                                                                   KULLA!
REPEAT
                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                      CHAIN
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193 GGGTAGGATAGGGAT GTAGGAG GLETAGAG GGGTAG HTATTAGT 1971 HT 24.2

or send an email to license list sib.ch).

EMBL: Y09392; CAA70561.1; -

CAA70559.1; CAA70560.1;

U72763; AAC50819. AAB41434.

Y09392; 083599; U83600; U78029;

Y09392;

U94501; AAC51306.1; U94504; AAC51309.1; U75380; AAC51392.1;

U74611; AAB39714.1;

AAB41435.1; AAB40918.1:

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MEDLINE—89096903. PubMad-2850481:
Sebgal A , Pafil N , Chao M ,
"A constitutive promoter directs expression of the nerve growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last angulation update)
LOW-ARE-2001 (Rel. 40, Last angulation update)
(GP80-LNGFR) (R75 ICD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87051725; PubMcd-3022937;
Johnson D., Lanahan A., Buck C.B., Sebgal A., Morgan C., Mercer E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Bominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NT-3, AND NT-4,
SHRUNIT: NGE BECEPTOR CAN FORM A HOMODIMEM THROUGH DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: LOW APPINITY RECEPTOR WHICH CAN BIND TO NGP, BONF,
                                                                                                                                          98 .nAlaSerClnValAlateuGluAsnCrsSerAlaValAtaAspThrArg 114
                                                                                                                                                                                                                                                                             460 GTGTG/ACCTGS/ATG/AGGTTC/TTT/AGAAAAAAAAGGGGTGTGT/CT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 rCysProThrSerThrLeuGlySerTysProflu.... ArgrysAlaA 193
                                   243 AGAAAACCACCTCAGA . CACTGCCTCAGCTGCTCCAAATGCCGAAAGG 289
                                                                                                          290 AAATGGGTOAGGGGGAAAD TOTTOTTGGGGGGGGAAGAGGGGAAAGAGAGAAG
                                                                                                                                                                                  GlnValSe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                    162 CysGlyThrCysLeuProGlyPheTyrGluHisGlyAspGlyCysValSe 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGTAACTGTAAGAGGCTGGAGTGCAGGA 544
                                                                                                                                                                                                                                                      TTCAATTTCAGCCTCTCTCAAAT G 421
65 CysclyAsnSerThrCysLeuValCysProGinAspThrPheLeuAlaTr 81
                                                                       81 pGluAsnHisHisAsnSerGluCysAlaArgCysGlnAlaCysAspGluG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression and structure of the human NGF receptor ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 AA
                                                                                                                                                                                                                    115 CyselyCystysProGlyTrpPhoValGluCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIO! 8-3160-3167(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: SwissProt_39:NGFR_NUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-22 PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S'TANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bothwell M., Chan M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BUND FURMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGFR OR TNFRSF16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 AGTTGTGC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 JaValCys 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606:
                                                                                                                                                                                                                                                                                                                                422 GGACCGTGCA...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      510 CTGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGFR_HUMAN
P08138;
                                                                                                                                                                                                                                                        390 CCAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) (POTENTIAL).
                                                                                                                                                                                                                                                                                         LOW-AFFINITY NERVE GROWTH FACTOR
                                                                                                                                                                                                                                                         Receptor, Neurogenėsis, Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 TGGAGATAGTGTGTGTCCCCAAGGAAATATATATOCACCTCAAAATAATT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 CGATTTGCTGCTACCAAGTGCCACAAAGGTACTTGTTGTACAATGACTGT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 CCACTGGTGCTGCTGGAGCTGTTGGTGGGAATATACCCCTCAGGGGTTAT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 ProArgLeuLeuLeuLeuLeuLeuClyValSerLeuGlyGly..... 27
                                                                                                                                                                                                                                                                                                    RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC ) (PO
B09FA143FB3D625B CKC64;
                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 194
Gaps: 12
Percent Identify: 31 443
                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: NGFR_HIMAN from: 1 to: 427
                                                                                                                                                                                                                                                                                                                                                 4 X TNFR-CYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AlaiysGluAlaCysProThrdlyLouTyrPhrHis
                                                                                                                                                                                                                                                                                                                                                                    TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEP/THP-PICH
                                                                                                                                                                                                                                                                                                                                                          TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                        DEATH.
                                                                                                                                                                                                                     PPOSITE: PSEGGE, TNFF_NGFF_1: 3.
PPOSITE: PSEGGEO; TNFP_NGFF_2: 4.
PROSITE: PSEGGI7; DEATH_DOMAIN: 1.
                                                                                                                                                Interpro: IPP000488; Death.
Interpro: IPR001368; TNFR_c6.
Pfam; PF00020; death; 1
SMAPT, SMO0005; TNFR_c6; 4.
SMART; SMO0008; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45183 MW;
                                                                                          EMBL, M14764; AARS9544.1; -. EMBL, M21621; AAA36363.1, -.
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HSSP; P07174; 1NGR.
MIM, 163010, -.
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Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.; "NMR structure of the death domain of the p75 neurotrophin receptor.";
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"Requilatory elements and transcriptional regulation by testostorone
and relinoir acid of the rat nerve growth lactor receptor promoter ";
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Mammalia, Eutheria, Rodentia, Scintognathi; Muridae, Murinae; Rattus
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01-APP-1988 (Rel. 07, East Scyucher update)
20 AUG-2001 (Rel. 46, East amediation update)
EGW-AFFINITY NEWVE GROWIH FATTOW REPETOP PRECUPSOR (NGF PROEPTOR)
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                                                                                  184 CHAGGCCCGGGGAAGGATAGGAAGGAAGGGGT GAGAGGGGGGTT 330
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                                                                                                                                      41 lyGluCysCysLysAlaCysAsnLeuGlyGluGlyValAlaGlnProCys 57
                                                                                                                                                                                                                                                                                                                           72 rPheSerAspValValSerAlaThrGluProCystysProCysThrGluC
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SEQUENCE OF 1-22 FROM N.A.
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ID NGFP_RAT STANDAPD;
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the European Bibliotofmatics Institute. There are no restrictions on its use by non-profit institutions as law as its content is in no way restricted and this statement is not removed. Sample by and for commercial whilities regulates a nicetise allocated (see bitter www istrict objancement) or send an email to license sible.
                                                                                                                 This SWISS-PRCT chttp is Oop/p ight. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
       -!- FUNCTION: LOW AFFILINIY RECEPTOR WHICH CAN BIND TO NSF, BONE.
N° 3, AND NF-4.
-!- SOBORTION OF RECEPTOR CAN FORM A HOMODIMER IMPOUGH DISULFIDE BOND FORMATION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- STMILAGLIF: C'ALCONTAINS A LA NOCHO, INSERINE.
-!- SIMILAGLIF: C'ALAND A LA NOCHO, INSERINE.
-!- SIMILAGLIF: C'ALAND A LA NOCHO, INSERINE-FICH REGION.
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EXTRACELLULAR (POTENTIAL).
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INFR-CYS 3.
INFR CYS 4.
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PROSITE: PSGGGSG; INFRINGER_2; 4.
PROSITE: PSGGGG; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                         NOT_ANNOIATED_CDS
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InterPro: IPR001368; INFR_c6.
Pfam: PF00531: death; 1.
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EMBO J. 16.4999 5005(1997).
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EMBL; X61269; -; NOI_ANNO
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"fumorigenic poxvituses, genomic organization and DNA sequence of the telomeric region of the Shope fibroma virus genome."; Virology 160-20-30(1987).
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Vituses, dsDNA vituses, no kNA stage, Poxvitidae; Chordopoxvilinae;
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Smith C.A., Davis T., Wignall J M . Din W.S . Parrah T , Upton C
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01-MAY-1992 (Rel. 22, Last Septence applate)
15-JUL-1992 (Rel. 38, Last annotation update)
TUMON NETROSIS FATION SOLURIE RETEPTOR PRECURSOR (PROFEIN T2)
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                                                                                                                                                                                                                                                                                                        GAGAGCGGCTTTCTAR 236
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                                                                                                                                                                                                                                                                                                      190 CCGGGGGPAGATACGGACTGCAGGGGGGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 TAACTGT.....
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McFadden G., Goodwin R.G.;
"T2 open reading frame from the Shope fibrema virus encodes a soluble
form of the TNP receptor ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
                                                                                           Biochem, Biophys, Res. Commun, 176:335-342(1991).
                                                                                                                                                                                      ANTIVIRAL EFFECTS OF THE CYTOKINE. SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                            REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 lyGlyHisAspTyr.....GluLysAspGlyLeuCysCysAlaSer 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Mct.LcuArg.LcuTleAlaLcuLcuValCysValValT;rValTyr.....
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51.232 Percent Identity: 29.064
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TNFR-CYS 3.
TNFR-CYS 4.
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PROSITE; PS5060; TNPR_NGFR_2; 1.
PROPERTO: Glynoprolein: Pepeat; Signal.
SIGNAL 1 16 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPP001368; INFP_c6.
Pfam; PF00020; INFP_c6. 2.
Probom; PF00077; INFC_c6; 1.
SMART; SMU0208; INFR; 3.
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HSSP; P19438; 1TNR.
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-91335768; Pubmed-1651597;
Upton C., Macen J.L., Schreiber M., McPadden G.;
Myxoma virus expresses a secreted protein with homology to the tumor
necrosis factor receptor gene lamily that contributes to viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myxoma virus (strain Lausanne).
Viruses: dsDNA viruses, no ENA staje, Poxviridae, Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VIFG1047 184-370-382(1941)
-1- FUNCTION: BINDS TO FNF-ALPHA AND RETA. PROBABLY PREVENTS TWF TO
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IUMOR NECEOSIS FACTOR SOLUBLE PECEPIOR PPECUPSOR (PROTEIN T2)
                                                       298 CAGGIGGAGAICICITTIEDACAGIGGAD PERGAMAMAGIGIGITG 347
                                                                                             GluSerGlnProCysAspArgThrHisAspArgValCysAsnCy 106
                                                                                                                                      348 CAGGAAGAACÇAGTAÇÇGÇETTATTĞGAGTGAAAAÇÇTTTTĞCAGTGCT 397
                                                                                                                                                                          106 sSerThrGlyAsnTyrCysLeuLeuLysGlyGlnAsn.....118
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                                                                                                                                                                                                                                                                                                                                        CAGAATGTTAAGGGCACTGAGGAGTGA 591
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seq_name: SwissProt_39:V12_MYXVL
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                                                                                                                                                                                    INFR-CYS 3.
                                                                                                                                                     INFR-CYS 1.
SMART: SM0208: TNFR: 3.
PRGSTI: PSGGGZ, TWFR_MGFL:: 2.
PRGSTIE: PSGGGSG: TNFR_NEFL:: 2.
PRGSTIE: PSGGGSG: TNFR_NEFL:: 3.
PRGSTIE: Glycopicited, Refeat. Glaual.
16.
PUTENITAL
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Ratio: 1.659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jonkins N.A., Smith C.A.; "Moltecular clouds and expression of the type 1 and type 2 murine receptors for tumon inectosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1- SIMILARITY: CONTAINS A LA-NGFP/(NEW-TYPF -YESTEINE-PICH PESSON
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodenia, Sciuroquathi: Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V., "Cloning and expression of CDNAs Lor two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kissonerghis M., Fellowes R., Feldmann M., Chernalovsky Y., Submitted (MAY-1995) to the PAHL/GonHank/DDH/ databases.
-!- FUNCTION: PERFERENCE FOR TNF-ALMA.
-!- SURCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.
ProAsnaluValVal 195
                                         CACTGCACCAACITE 548
                                                                             196 LysThrSerGluPheSerValThrLeuAsnHisThrAspCysAspPrcVa 212
                                                                                                                                                                                                                                                                                                                  01-MAY-1992 (Rel. 22) Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSTS FACTOR RECEPTOR 2 PRECURSOR (INE-R2) (P75).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacob C.O., Liu J.;
Submitted (IAN-1996) to the PMRL/GERBARE/APPRE databases
                                                                                                                  549 GTGCCTACCCANATTRANAAATGTTAAGGACACACTGAGGCTCAGGC 594
                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991)
                                                                                                                                                                                                                                                            474 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-91246168; PubMed-1645445;
                                       508 TCCTGTAGTAACTGTAAGAAAAGGCTG
                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rgl. 22, Created)
01-MAY-1992 (Rgl. 22, Last sequ
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Ptam, PF00020; TNFR :4.
                                                                                                                                                                                                 seq_name: SwissProt_39:TNR2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                 INFRSFIB OR TNFRZ OR TNFR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 039488; AAA85021.1: -; X87128; CAA60618.1; -; B38634; H38634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M60469; AAA39752.1; -. EMBL; M59378; AAA40463.1; -.
183 hrSerCysThrThrThrAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD: MGI:1314883; Infrsflb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1.22 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-26 FROM N.A.
                                                                                                                                                                                                                                                            FNR2_MOUSE STANDARD;
P25119; P97893;
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P19438; INCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOUFNCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIKAIN-NOD;
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. .) (POTENTIAL).
                                                                                                                                                   TUMOR NECPOSIS FACTOR RECEPTOR 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 | IATaSerSerArgAlaProAsnGlyAsnValLeuCystysAlaCysAlaP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 CAAGTGGGACAAAAGAAAGTAACTTGTAAAATGACTGCTGCGGGGG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 AsmilaBbeArgThr/ysLeuSerCysSerSerSerSerTysThrAsp., 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGCATTATTGGAGTGAA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 laCysCluAlaClyArgTyrCysAlaLeuLysThrHis.....SerCly 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 AACCTTTTCCAGTGCTTCAATTGCAGGCTCTGGCTCAATGGG...AGCGT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 COACCITCLICCLICCCAGGAGAACAGAACAOOGIGIOT...ACCITGCCAIG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 CysGlnIleSerGlnGluTyrTyrAspArgLysAlaGlnMetCysCysAl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 erAspThrValCysAlaAspCysGluAlaSerMetTyrfhrGlnValTrp 88
                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462FAF 19804IN5561 CRC64;
                                                                                                  Transmembrane, Glycoprotein, Repeat, Signal.
                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC.
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TNFR-CYS 4.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                               4 X TNFR-CYS.
                                                                                                                                                                                                                                                                       TNFR-CYS 1.
                                                                                                                                                                                                                                                                                                TNFR-CYS 2.
       PRODUIL FEWERS TARRY 4.
SMART, SM00208; TNFR, 4.
PROSTTE; PS00652; TNFR_NGFR_1; 2.
PROSTTE: FS00652; TNFR_NGFR_2; 3.
                                                                        TNFR_NCFR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50319 MW;
Probom; PD000771; TNFR_c6; 1.
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US-09-525-998A-11 x TNR2_MOUSE
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474 AA;
                                                                          PS50050;
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Ratio:
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39
78
120
165
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                                                                                                    Receptor,
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                                                                          PROSTTE;
                                                                                                                                                                                                 FRANSMEM
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REPEAT
REPEAT
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476 CAGGITICTIFCTAAGAGAAAAQGAGTGICTCCCCGCAGTAACTGTAAG 525

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA, POSSIBLE FUNCTION IN IMMONE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Force W.R., Waiter B.N., Besslow C., Fizard F., Kezak C.A.,
Browning J.L., Ware C.F.,
"Mouse lymphotoxin beta receptor. Molecular genetics, ligand binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The murine lymphotoxin beta receptor CDNA: isolation by the signal sequence frap and chromosomal mapping."; Genomics 30:312-319(1995).
                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota: Metarea: Cherdata; Craniata: Vertetrata, Euteleestemi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·!- SIMILARITY: CONTAINS A LA-NGER/THER-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŚEQUENCE FROM N.A.
MEDLINE-96163885; PubMed-8586432;
Nakamura T., Tashiro K., Nazaréa M., Nakano T., Sasayama S.
168 rodlyThrPhc.....SerAspThrThrSerSerThrAspValCysArg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Receptor: Transmentane: Siyroptotein; Repeat; Signal. | 30 | POTENTIAL. | 1 | 415 | POTENTIAL. | CHAIN | 31 | 223 | EXHRACELULAR (POTENTIAL). | IRANSMEM | 224 | 244 | POTENTIAL. | POTENTIAL. | LOMAIN | 245 | 415 | CYTOPIASMIC (POTENTIAL). | DOMAIN | 245 | 415 | CYTOPIASMIC (POTENTIAL). | DOMAIN | 2 | 213 | 4 | X | TNFR CYS. | REPEAT | 42 | 81 | TNFR-CYS. | REPEAT | 82 | 2.24 | TNFR-CYS. | REPEAT | 15 | 170 | TNFR-CYS. 3. | REPEAT | 171 | 213 | TNFR-CYS. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                         526 ANANGCCIGGAGIGCACGAAGIIGITGIGCCIACCC 558
                                                                             183 ProHisArgileCysSerlleLeuAlallePro 193
                                                                                                                                                                                                                                                                            LYMPHOTOXIN-BEIA RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJINE-96072804; PubMed-7594541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART: SMOODOR; INFK; 3
PROSITE; PSOO652; FNFR_NGFR_1; 2,
PPOSITE; PS50050; INFP_NGFR_2; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol, 155:5280 5288(1995).
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Made; MC104875; Lithr
InterPro; IPR001368; TNFR_r6.
Plam; PF00020; TNFR_r6. r
ProDom; PD000771; TNFR_c6; 1.
                                                                                                                      seq_name: SwissProt_39:INRC_MOUSE
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                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE-Lung;
                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and expression."
                                                                                                                                                                                                                                                                                               LIBE OF INFOR.
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                                                                                                                                                                          INPC_MOUSE
P50294;
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CVB;
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LIBRED (GENAC: ...) (PATENTIAL).
LIBRED (GENAC: ...) (PATENTIAL).
29H324A56AFF561 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 IGCTGTAPMAGTGCPACAAAGGAACCTACTIGIACAATGAPTGIGGGAGG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 CACTIONATOMAGGIIINTIINGIAAGAAAAQGAGIINTIINGIA 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 uleuValAlaSerdlnProGlnLeuValProProlytArylleGluAsnG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4] infludystipAspdinAsplysdiblyrtyrdinProMetHisAspVal 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 CysCysSerAidCysFioProdlyGluPheValPheAldValCys...Se 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 JILCAGAAAASTACICAGACACIGGLICAGCIGCIGCIACAAAI s.CGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 GAAATGGGTCAGGTGGAGATGTTTTTTGCACAGGACGGGACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 udyski i jasladioflyMetserdysVallyrieuAspAsmin
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1,714 Gaps: 9
19,763 Evillat DAnatity, 28,915
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US:09 525-998A-11 x INRC_MGSE
      Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a lictuse agreement (see http://www.isb sib.ch/announce/
or send an email to licensegisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUNICACIOLINE OF PAGE TO THE EMBL/GenBank/DDBJ databases.

FINCTION: PECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASE. THE ADAPTOR MOLECULE FADD RECKUIS CASPASE B 10 THE ACTIVATED RECEPTOR. THE RESOLUTING AGGREGATE CALLED THE DEATH-INDICING SIGNALING COMPLEX (DISC) PERFORMS CASPASE B PROTECULY CASPASE A ACTIVATION. ACTIVATION. ACTIVATION. ACTIVATION. ACTIVATION. ACTIVATION. ACTIVATION OF PRECIFIC CYSTEINE PROTECASES) MEDIATING APOPTOSIS. FAS MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERPINHERAL TOLERANCE, IN THE ANTIGRA-STIMULATED SULCINE OF MATURE TELLS, PORTORING THE AUGUST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bart ing B., Hoffmann I., Holtz J., Schulz B., Househ C., Darmer D.; "Mixtession of apoptosis associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN. CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD. AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -t- SIMILAFITY: CANTAINS A LA-NAFF/INFK-TYPE AYSTEINE-RICH RESTON.
-t- SIMILARITY: CONTAINS I DEATH DOMAIN.
                                                                                                                                                                                                                                                                                            15-UUL-1999 (Ref. 38, Last sequence update)
20-AUG-2001 (Ref. 40. Last annotation update)
FASE PECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Cramiata, Vertebrata, Euteleostomi;
Mammalia: Eutheria: Cerarifodamiyla: Suiba, Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane, Repeat, Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
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                              200 SluAlaAlaProS!;?hrserNyrSerAspThr 210
565 GAGAATGTTAAGGGCACTGAGGACTCAGGCACC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFR-CYS 3.
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16 POTENTIAL
                                                                                                                                                                                                     PRT;
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DPOSTIF: PSSGONSO: TNPP_NOPP_2: 2
PROSTIE: PSSGON7: DMATH_DOMAIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ001202; CAA04596.1; ...
InterPro; IPR000488; Death.
InterPro; IPR001368; TWFF_c6.
                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 3.
                                                                                                                  Seq_name SwissProt_39:FASA_PIG
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                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                   (APO-1 ANTIGEN) (CD95).
TWFRSF6 OR APT1 OR FAS.
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SIGNAL 1
                                                                                                                                                                             seq_documentation_block
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227
38
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
CD401. PECEPTOR PRECURSOR (R-CELL SURFACE ANTIGEN CD40) (FMAGMENT)
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Mammalla, Eutheria, Cetartiodactyla, Ruminantia, Perora, Boyoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 97281252; PubMed-9135560:
Hirano A., Brown W.C., Estes D.M.;
"Cloning, expression and biological function of the bovine CD40
homelogue: role in B-lymphocyte growth and differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 GATAGTGTGTGTGTGTGTGTGTAAAAATATATATGCACCCTCAAAATAATTCGAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 pGlyGluHisGlyLeuGluValGluLysAsnCysThrArqThrGlnAsnT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **5 POSTGIGIGIGINTGPAGARGARCARCAGIACOGRATIALIGIGAGIGAAAAC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 hrlysCysAigCysLysProAsnPhePheCysHis....ThrSerGln 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 INTITIONAL GATE OF A TRANSPORTED TO THE CARD OF STORY OF A 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 TTGCTGTAPPAAGTGPPAAAAGAAPPTAPTTGTAGAATGAGTGTGCAG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 ACCGCTTCAGAAAACCACCTCAGACTGCCTCAGCIGCTCCAAATGCCG 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 eCysCysGlnProCysProProGlyLysAiqLysHisAlaAspCysThrS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgeluslysinPh 56
                                                                                                                              Percent Identity: 29.134
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                                        Length:
                                                                                                Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: FASA_PIG from: 1 to: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 CTCCTGCCAGGAGAACAGAACACGTGTGC 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 GluserGludysProGluGlyGlnHis
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                                                                                                                                                                                                                                                                                 US-09-525-998A-11 x FASA_PIG
                                   176.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyinac, Hos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax1D-9913;
                                             Quality.
                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFRSF5 OR CD40.
                                                                                                                              Percent Similarity:
alignment_scores:
                                                                                                                                                                                                                                   alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boyridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cattle.
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                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                  61yeprotein; Transmembrane; Repeat; Signal.
19 POTENTIAL.
>269 CD40L RECEPTOR.
                                                                                                                                                                          CD401 RECEPTOR, EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                       29983 MW; 746903F30F95F387 CRC64;
                                                                                                                                                                                                  POTENTIAL. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                          4 X INFR-CYS.
TNFR-CYS 1.
INFR-CYS 2.
                                                                                                                                                                                                                                                             INFR-CYS 3.
INFR-CYS 4.
                                                                                                                             PROSITE: PSOO652: TNFR_NGFR_1: 1. PROSITE: PS50050: TNFR_NGFR_2: 1. Receptor: B-cell: Glycoprotein: T
                                                                            nass, F. 1989 (1988) TNFR_C6.
Pram: PF00020: TNFR_C6: 4.
Protxm: PD000771: TNFR_C6: 1
                                                           EMBL: 057745, AAC48710.1;
                                                                                                                   SMARF; SM00208; TNFR; 4.
                                                                                                                                                                                       193
215
>269
                                                                        CDF.
                                                                                                                                                                                                                                                                                                                      269 AA;
                                                                                                                                                                            20
20
194
216
                                                                      P25942;
                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                                                                    ARBOHYD
                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                      SHOURNCE
                                                                                                                                                                            CHAIN
                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                            NON LEE
                                                                                                                                                                                                                                     KEPEAI
KEPEAT
                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                             KEPEA1
                                                                                                                                                                                                                                                                       REPEAT
```

Align seg 1/1 to: CD40_BOVIN from: 1 to: 269

 17 aValHisSerGiuProAlathrAlaCysGluGiysGluTyrProVal. 33

78 OCTIANIGGAGATACHGIGICCCCAAGGAAAATAHAICCACCCTCAAA 127

128 AINATICGATIIGCIGIACCAAGIGCCACAAAGGAAGGIACIIGIAGAAI 177

34 ...AsmSerLeuCysCysAspleuCysProPredIyClnLysLeuValAsm 49

65 yGluPheLeuSerThrTrpAsnArgGluLysTyrCysHisGluHisArgT 82

 328 GGGGACACCCPGTGGCTGCAGGAAGCAGCACTACCGGCATTATTGGAG 377 | 11111:::111 | 111 | :::::111 | 111

99 ThrAspThrIleCysValGysValGluGlyGln.....HisCysThrSe 113

.